

AMENDMENTS TO THE CLAIMS

Please incorporate the following amendments to the subject application.

In the Claims:

1. **(Currently Amended)** A method of identifying a region of a genome of a cell to which a protein of interest binds, comprising the steps of:
 - a) crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
 - b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
 - c) removing a DNA fragment to which the protein of interest is bound from the mixture produced in b);
 - d) separating the DNA fragment identified in c) from the protein of interest;
 - e) amplifying the DNA fragment of d);
 - f) combining the DNA fragment of e) with a DNA microarray comprising ~~one or more~~ **than one** sequence[[s]] complementary to ~~one or more~~ **than one** intergenic region[[s]] **of more than one transcribed region** of genomic DNA of the cell wherein each ~~one or more~~ sequence[[s]] is located at a particular spot on the DNA microarray and ~~the one or more intergenic regions are upstream of transcribed regions of the genomic DNA is an intergenic fragment, wherein the sequences are across a portion of the genome of the cell, under conditions in which hybridization between the DNA fragment and the ~~one or more~~ sequences complementary to ~~one or more~~ **the** intergenic regions of the genomic DNA occurs; and~~
 - g) identifying the ~~one or more~~ sequences complementary to the ~~one or more~~ intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes,

whereby the region identified in g) is the region of the genome in the cell to which the protein of interest binds and the portion of the genome is examined to determine where the protein of interest binds.

2. (Original) The method of Claim 1 wherein the cell is a eukaryotic cell.
3. (Original) The method of Claim 1 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.
4. (Original) The method of Claim 1 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.
5. (Original) The method of Claim 1 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.
6. (Original) The method of Claim 1 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.
7. Canceled.
8. **(Currently Amended)** The method of Claim 1 further comprising:
h) comparing the ~~one or more~~ the sequences identified in g) with a control.
9. **(Currently Amended)** A method of identifying a region of a genome of a cell to which a protein of interest binds, comprising the steps of:
 - a) formaldehyde crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
 - b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing DNA fragments to which DNA binding protein is bound;

- c) immunoprecipitating the DNA fragment produced in b) to which the protein of interest is bound using an antibody that specifically binds the protein of interest;
- d) separating the DNA fragment identified in c) from the protein of interest;
- e) amplifying the DNA fragment of d) using ligation-mediated polymerase chain reaction;
- f) fluorescently labeling the DNA fragment of e);
- g) combining the labeled DNA fragment of ~~[[e)]]~~ f) with a DNA microarray comprising ~~one or more~~ than one sequence~~[[s]]~~ complementary to ~~one or more~~ than one intergenic region~~[[s]]~~ of more than one transcribed region of genomic DNA of the cell wherein each ~~one or more of the~~ sequences is located at a particular spot on the DNA microarray and ~~the one or more intergenic regions are upstream of transcribed regions of the genomic DNA is an intergenic fragment, wherein the sequences are across a portion of the genome of the cell,~~ under conditions in which hybridization between the DNA fragment and the ~~one or more~~ the sequences complementary to the ~~one or more~~ the intergenic regions of genomic DNA occurs;
- h) identifying the ~~one or more~~ sequences complementary to the ~~one or more~~ intergenic regions of genomic DNA to which the DNA fragment hybridizes by measuring fluorescence intensity of the hybridized DNA fragment; and
- i) comparing the fluorescence intensity measured in h) to the fluorescence intensity of a control,
whereby fluorescence intensity in a region of the genome which is greater than the fluorescence intensity of the control in the region indicates the region of the genome in the cell to which the protein of interest binds and the portion of the genome is examined to determine where the protein of interest binds.

10. (Currently Amended) A method of determining a function of a protein of interest which binds to a genome of a cell, comprising the steps of:

- a) crosslinking DNA binding protein in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
- c) removing the DNA fragment to which the protein of interest is bound from the mixture produced in b);
- d) separating the DNA fragment identified in c) from the protein of interest;
- e) amplifying the DNA fragment of d);
- f) combining the DNA fragment of e) with a DNA microarray comprising ~~one or more~~ than one sequence~~[[s]]~~ complementary to ~~one or more~~ than one intergenic region~~[[s]]~~ of more than one transcribed region of genomic DNA of the cell wherein each ~~one or more~~ of the sequences is located at a particular spot on the DNA microarray and ~~the one or more intergenic regions are upstream of transcribed regions of the genomic DNA is an intergenic fragment, wherein the sequences are across a portion of the genome of the cell~~, under conditions in which hybridization between the DNA fragment and the ~~one or more~~ the sequences complementary to ~~one or more~~ the intergenic regions of the genomic DNA occurs;
- g) identifying the ~~one or more~~ sequences complementary to the ~~one or more~~ intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes; and
- h) characterizing the ~~one or more~~ sequences identified in g), wherein the characteristics of the ~~one or more~~ the sequences of h) indicate a function of the protein of interest which binds to the genome of the cell and the portion of the genome is examined to determine where the protein of interest binds.

11. (Currently Amended) A method of determining whether a protein of interest which binds to the genome of a cell functions as a transcription factor, comprising the steps of:

- a) crosslinking DNA binding protein in the cell to the genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA;
- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound;
- c) removing the DNA fragment to which the protein of interest is bound from the mixture produced in b);
- d) separating the DNA fragment identified in c) from the protein of interest;
- e) amplifying the DNA fragment of d);
- f) combining the DNA fragment of e) with a DNA microarray comprising ~~one or more~~ than one sequence~~[[s]]~~ complementary to ~~one or more~~ than one intergenic region~~[[s]]~~ of more than one transcribed region of genomic DNA of the cell wherein each ~~one or more of the~~ sequences is located at a particular spot on the DNA microarray and ~~the one or more intergenic regions are upstream of transcribed regions of the genomic DNA is an intergenic fragment, wherein the sequences are across a portion of the genome of the cell,~~ under conditions in which hybridization between the DNA fragment and the ~~one or more the~~ sequences complementary to ~~one or more the~~ intergenic regions of the genomic DNA occurs; and
- g) identifying the ~~one or more~~ sequences complementary to the ~~one or more~~ intergenic regions of the genomic DNA of f) to which the DNA fragment hybridizes, wherein if the ~~one or more the~~ sequences complementary to genomic DNA of g) is a regulatory region, then the protein of interest is a transcription factor and the portion of the genome is examined to determine where the protein of interest binds.

Claims 12-14. (Canceled)

15. (Previously Presented) The method of Claim 1 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

16. (Previously Presented) The method of Claim 15 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

17. (Previously Presented) The method of Claim 1 wherein the DNA fragments are generated using shearing conditions.

18. **(Currently Amended)** The method of Claim 1 wherein the ~~one or more~~ **the** intergenic regions of genomic DNA in g) comprises a regulatory region.

19. (Previously Presented) The method of Claim 18 wherein the regulatory region comprises a promoter region.

20. (Previously Presented) The method of Claim 19 wherein the promoter region comprises a promoter for two divergently transcribed genes.

21. **(Currently Amended)** The method of Claim 1 wherein the ~~one or more~~ **the** intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.

22. **(Currently Amended)** The method of Claim 1 wherein the ~~one or more~~ **the** intergenic regions of genomic DNA in g) is a binding site for a transcriptional activator.

23. **(Currently Amended)** The method of Claim 1 wherein the ~~one or more~~ **the** intergenic regions of genomic DNA in g) is a binding site for a cell cycle transcription factor.

24. (Previously Presented) The method of Claim 23 wherein the cell cycle transcription factor regulates one or more genes selected from the group

consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.

25. (Previously Presented) The method of Claim 9 wherein the cell is a eukaryotic cell.

26. (Previously Presented) The method of Claim 9 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.

27. Canceled.

28. (**Currently Amended**) The method of Claim 9 further comprising:
j) comparing the ~~one or more~~ sequences identified in h) with a control.

29. (Previously Presented) The method of Claim 9 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

30. (Previously Presented) The method of Claim 29 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

31. (Previously Presented) The method of Claim 9 wherein the DNA fragments are generated using shearing conditions.

32. (**Currently Amended**) The method of Claim 9 wherein the ~~one or more~~ intergenic regions of genomic DNA in h) comprises a regulatory region.

33. (Previously Presented) The method of Claim 32 wherein the regulatory region comprises a promoter region.

34. (Previously Presented) The method of Claim 33 wherein the promoter region comprises a promoter for two divergently transcribed genes.

35. **(Currently Amended)** The method of Claim 9 wherein the ~~one or more~~ intergenic regions of genomic DNA in h) comprises a consensus DNA binding region.

36. **(Currently Amended)** The method of Claim 9 wherein the ~~one or more~~ intergenic regions of genomic DNA in h) is a binding site for a transcriptional activator.

37. **(Currently Amended)** The method of Claim 9 wherein the ~~one or more~~ intergenic regions of genomic DNA in h) is a binding site for a cell cycle transcription factor.

38. **(Previously Presented)** The method of Claim 37 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.

39. **(Previously Presented)** The method of Claim 10 wherein the cell is a eukaryotic cell.

40. **(Previously Presented)** The method of Claim 10 wherein the protein of interest is selected from the group consisting of: a transcription factor and an oncogene.

41. **(Previously Presented)** The method of Claim 10 wherein the DNA binding protein of the cell is crosslinked to the genome of the cell using formaldehyde.

42. **(Previously Presented)** The method of Claim 10 wherein the DNA fragment of c) to which is bound the protein of interest is identified using an antibody which binds to the protein of interest.

43. (Previously Presented) The method of Claim 10 wherein the DNA fragment of e) is amplified using ligation-mediated polymerase chain reaction.

44. Canceled.

45. (Previously Presented) The method of Claim 10 further comprising:
i) comparing the region identified in g) with a control.

46. (Previously Presented) The method of Claim 10 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

47. (Previously Presented) The method of Claim 46 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

48. (Previously Presented) The method of Claim 10 wherein the DNA fragments are generated using shearing conditions.

49. **(Currently Amended)** The method of Claim 10 wherein the ~~one~~
~~or more~~ intergenic regions of genomic DNA in g) comprises a regulatory region.

50. (Previously Presented) The method of Claim 49 wherein the regulatory region comprises a promoter region.

51. (Previously Presented) The method of Claim 50 wherein the promoter region comprises a promoter for two divergently transcribed genes.

52. **(Currently Amended)** The method of Claim 10 wherein the ~~one~~
~~or more~~ intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.

53. **(Currently Amended)** The method of Claim 10 wherein the ~~one~~
~~or more~~ intergenic regions of genomic DNA in g) is a binding site for a
transcriptional activator.

54. **(Currently Amended)** The method of Claim 10 wherein the ~~one~~
~~or more~~ intergenic regions of genomic DNA in g) is a binding site for a cell cycle
transcription factor.

55. **(Previously Presented)** The method of Claim 54 wherein the cell
cycle transcription factor regulates one or more genes selected from the group
consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination
thereof.

56. **(Previously Presented)** The method of Claim 11 wherein the cell is a
eukaryotic cell.

57. **(Previously Presented)** The method of Claim 11 wherein the DNA
binding protein of the cell is crosslinked to the genome of the cell using
formaldehyde.

58. **(Previously Presented)** The method of Claim 11 wherein the DNA
fragment of c) to which is bound the protein of interest is identified using an antibody
which binds to the protein of interest.

59. **(Previously Presented)** The method of Claim 11 wherein the DNA
fragment of e) is amplified using ligation-mediated polymerase chain reaction.

60. Canceled.

61. **(Previously Presented)** The method of Claim 11 further comprising:
h) comparing the region identified in g) with a control.

62. (Previously Presented) The method of Claim 11 wherein after the DNA fragment is separated from the protein of interest, the DNA fragment is labeled with a fluorescent dye.

63. (Previously Presented) The method of Claim 62 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

64. (Previously Presented) The method of Claim 11 wherein the DNA fragments are generated using shearing conditions.

65. (Previously Presented) The method of Claim 11 wherein the regulatory region comprises a promoter region.

66. (Previously Presented) The method of Claim 65 wherein the promoter region comprises a promoter for two divergently transcribed genes.

67. **(Currently Amended)** The method of Claim 11 wherein the ~~one or more~~ intergenic regions of genomic DNA in g) comprises a consensus DNA binding region.

68. **(Currently Amended)** The method of Claim 11 wherein the ~~one or more~~ intergenic regions of genomic DNA in g) is a binding site for a transcriptional activator.

69. **(Currently Amended)** The method of Claim 11 wherein the ~~one or more~~ intergenic regions of genomic DNA in g) is a binding site for a cell cycle transcription factor.

70. (Previously Presented) The method of Claim 69 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.

71. **(Currently Amended)** A method of identifying regions across a genome of a cell where binding of DNA binding proteins occurs, comprising the steps of:

- a) crosslinking DNA binding proteins in the cell to genomic DNA of the cell, thereby producing DNA binding proteins crosslinked to genomic DNA;
- b) generating DNA fragments of the genomic DNA crosslinked to DNA binding proteins in a), thereby producing a mixture comprising DNA fragments to which DNA binding proteins are bound;
- c) removing DNA fragments to which the DNA binding proteins are bound from the mixture produced in b);
- d) separating the DNA fragments identified in c) from the DNA binding proteins;
- e) amplifying the DNA fragments of d);
- f) combining the DNA fragments of e) with DNA comprising **more than one** sequence~~[[s]]~~ complementary to intergenic regions **of more than one transcribed region** of genomic DNA of the cell **wherein each of the sequences complementary to intergenic regions of genomic DNA of the cell are intergenic fragments and are across a portion of the genome of the cell**, under conditions in which hybridization between the DNA fragments and the sequences complementary to the intergenic regions of the genomic DNA occurs; and
- g) identifying the sequences complementary to the intergenic regions of genomic DNA of f) to which the DNA fragments hybridize, whereby the regions identified in g) are regions across the genome of the cell where binding of DNA binding proteins occur **and the portion of the genome is examined to determine where the protein of interest binds.**

72. **(Previously Presented)** The method of Claim 71 wherein the cell is a eukaryotic cell.

73. (Previously Presented) The method of Claim 71 wherein the DNA binding proteins of the cell are crosslinked to the genome of the cell using formaldehyde.

74. (Previously Presented) The method of Claim 71 wherein the DNA fragments of c) to which are bound DNA binding proteins are identified using antibodies which bind to the DNA binding proteins.

75. (Previously Presented) The method of Claim 71 wherein the DNA fragments of e) are amplified using ligation-mediated polymerase chain reaction.

76. (Previously Presented) The method of Claim 71 further comprising:
h) comparing the sequences identified in g) with a control.

77. (Previously Presented) The method of Claim 71 wherein after the DNA fragments are separated from the DNA binding proteins, the DNA fragments are labeled with a fluorescent dye.

78. (Previously Presented) The method of Claim 77 wherein the fluorescent dye is selected from the group consisting of: Cy5 and Cy3.

79. (Previously Presented) The method of Claim 71 wherein the DNA fragments are generated using shearing conditions.

80. (Previously Presented) The method of Claim 71 wherein the intergenic regions of genomic DNA in g) comprise a regulatory region.

81. (Previously Presented) The method of Claim 80 wherein the regulatory region comprises a promoter region.

82. (Previously Presented) The method of Claim 81 wherein the promoter region comprises a promoter for two divergently transcribed genes.

83. (Previously Presented) The method of Claim 71 wherein the intergenic regions of genomic DNA in g) comprise a consensus DNA binding region.

84. (Previously Presented) The method of Claim 71 wherein the intergenic regions of genomic DNA in g) comprise a binding site for a transcriptional activator.

85. (Previously Presented) The method of Claim 71 wherein the intergenic regions of genomic DNA in g) comprise a binding site for a cell cycle transcription factor.

86. (Previously Presented) The method of Claim 85 wherein the cell cycle transcription factor regulates one or more genes selected from the group consisting of: G1 genes, G2/M genes, M/G1 genes, G1/S genes and a combination thereof.

Please enter the following new claims:

87. (New) The method of Claim 1 further comprising:
(h) identifying a DNA binding site of the protein of interest in the region identified in g) wherein the protein of interest is a transcription factor.

88. (New) The method of Claim 1, wherein said sequences are across a chromosome and the chromosome is examined to determine where the protein of interest binds.

89. (New) The method of Claim 92, wherein said sequences are across an entire genome the entire genome is examined to determine where the protein of interest binds.

90. (New) The method of Claim 1, wherein said amplifying comprises non-specifically amplifying.

91. (New) The method according to Claim 90, wherein said non-specifically amplifying is by ligation-mediated polymerase chain reaction (LM-PCR).

92. (New) The method according to Claim 1, wherein said array contains spots representing all of the genome of said cell.